

United States Patent and Trademark
Scientific and Technical Information Center
Biotechnology Systems Branch

FAX TRANSMISSION COVER SHEET

DATE: 08-31-2005

Total Number of Pages Faxed: 8 (COV. INCL)

TO:

NAME: Ahmed, Shateel

ORG.: _____

FAX NUMBER: 703-305-3230

FROM: Mark Spencer

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Message:

Re- s/n 10/501,675

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/501, 675
Source: PCT
Date Processed by STIC: 08/31/2005

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/501,675

DATE: 08/31/2005

TIME: 15:00:16

Input Set : A:\03-004 SEQUENCE LISTING.txt

Output Set: N:\CRF4\08312005\J501675.raw

3 <110> APPLICANT: TANABE SEIYAKU CO., LTD.
5 <120> TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.
7 <130> FILE REFERENCE: 03-004-PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/501,675
C--> 9 <141> CURRENT FILING DATE: 2004-07-16
9 <150> PRIOR APPLICATION NUMBER: JP2002-008435
10 <151> PRIOR FILING DATE: 2002-01-17
12 <160> NUMBER OF SEQ ID NOS: 11
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 21
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Artificially synthesized primer sequence
24 <400> SEQUENCE: 1
25 gttttccag tcacgacgtt g 21
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 21
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Artificially synthesized primer sequence
36 <400> SEQUENCE: 2
37 accatgatta cgccaagctt g 21
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 18
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Artificially synthesized primer sequence
48 <400> SEQUENCE: 3
49 tgtaaaacga cggccagt 18
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 87
54 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 4
58 gatcatgttg ttttgcgtg tattttatta atgtactcta ttgcattaat tggtttttgg 60
60 atattaaacc aactttgcat tcctaaa 87
63 <210> SEQ ID NO: 5
64 <211> LENGTH: 21
65 <212> TYPE: DNA

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68 <220> FEATURE:
69 <223> OTHER INFORMATION: Artificially synthesized primer sequence
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75 <210> SEQ ID NO: 6
76 <211> LENGTH: 25
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Artificially synthesized primer sequence
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84 gtccagcgca gccccgcaga gctcc                               25
87 <210> SEQ ID NO: 7
88 <211> LENGTH: 25
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Artificially synthesized primer sequence
95 <400> SEQUENCE: 7
96 aaatacacga caaaaccaca tgate                               25
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 3587
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
104 <220> FEATURE:
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (99)..(2552)
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111 gcaagggctg ggccctggagt gaagctggaa gggctagc atg gag agc ctg tca cct 116
112                                     Met Glu Ser Leu Ser Pro
113                                     1           5
115 ggg gga cca act ggc cac cct tac cag ggg gag gcc tct acc tgc tgg 164
116 Gly Gly Pro Thr Gly His Pro Tyr Gln Gly Glu Ala Ser Thr Cys Trp
117          10           15           20
119 cag ctc aca gtg agg gtc ctg gag gcg cgg aac ctg cgc tgg gct gac 212
120 Gln Leu Thr Val Arg Val Leu Glu Ala Arg Asn Leu Arg Trp Ala Asp
121          25           30           35
123 ctg ttg agt gag gcc gac cct tac gtg atc cta cag ctg tcg acc gca 260
124 Leu Leu Ser Glu Ala Asp Pro Tyr Val Ile Leu Gln Leu Ser Thr Ala
125          40           45           50
127 cct gga atg aag ttt aag acc aag acg ctc acc gac acc agt cat cct 308
128 Pro Gly Met Lys Phe Lys Thr Lys Thr Leu Thr Asp Thr Ser His Pro
129          55           60           65           70
131 gtg tgg aat gag gcc ttc cgt ttc ctt atc caa agt cag gtc aag aat 356
132 Val Trp Asn Glu Ala Phe Arg Phe Leu Ile Gln Ser Gln Val Lys Asn
133          75           80           85
135 gtt ctg gag ctt agc atc tat gat gag gac tca gtc acg gag gat gac 404

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136	Val	Leu	Glu	Leu	Ser	Ile	Tyr	Asp	Glu	Asp	Ser	Val	Thr	Glu	Asp	Asp	
137				90					95					100			
139	atc	tgc	ttc	aag	gtt	ctc	tat	gac	atc	tca	gaa	gtc	ctc	cct	ggc	aag	452
140	Ile	Cys	Phe	Lys	Val	Leu	Tyr	Asp	Ile	Ser	Glu	Val	Leu	Pro	Gly	Lys	
141			105					110					115				
143	ctg	ctc	egg	aaa	acc	ttc	tcc	cag	agt	ccc	cag	gga	gag	gag	gag	ctg	500
144	Leu	Leu	Arg	Lys	Thr	Phe	Ser	Gln	Ser	Pro	Gln	Gly	Glu	Glu	Glu	Leu	
145		120					125					130					
147	gat	gtg	gag	ttc	ctg	atg	gaa	gaa	acg	tca	gat	cgc	cca	gaa	aac	ctc	548
148	Asp	Val	Glu	Phe	Leu	Met	Glu	Glu	Thr	Ser	Asp	Arg	Pro	Glu	Asn	Leu	
149	135					140				145					150		
151	atc	acc	aac	aaa	gtc	att	gtg	gcc	cga	gag	ctg	tca	tgc	ctg	gat	gtg	596
152	Ile	Thr	Asn	Lys	Val	Ile	Val	Ala	Arg	Glu	Leu	Ser	Cys	Leu	Asp	Val	
153				155					160					165			
155	cat	ctg	gac	agc	aca	ggg	agc	acc	gct	gtg	gtt	gca	gat	cag	gac	aag	644
156	His	Leu	Asp	Ser	Thr	Gly	Ser	Thr	Ala	Val	Val	Ala	Asp	Gln	Asp	Lys	
157			170					175					180				
159	ctg	gag	ctg	gag	ctg	gtg	ctg	aag	ggg	tcc	tat	gag	gac	aca	cag	aca	692
160	Leu	Glu	Leu	Glu	Leu	Val	Leu	Lys	Gly	Ser	Tyr	Glu	Asp	Thr	Gln	Thr	
161		185					190					195					
163	tcc	ttc	ctg	ggc	aca	gcc	tct	gcc	ttc	cgc	ttc	cac	tac	atg	gca	gcc	740
164	Ser	Phe	Leu	Gly	Thr	Ala	Ser	Ala	Phe	Arg	Phe	His	Tyr	Met	Ala	Ala	
165		200				205					210						
167	cta	gag	aca	gag	ctg	agc	ggg	cgc	ctg	agg	agc	tcc	aga	agc	aat	ggc	788
168	Leu	Glu	Thr	Glu	Leu	Ser	Gly	Arg	Leu	Arg	Ser	Ser	Arg	Ser	Asn	Gly	
169	215					220				225					230		
171	tgg	aat	ggg	gac	aac	tca	gct	ggg	tac	ctc	act	gtg	ccc	ctg	agg	ccc	836
172	Trp	Asn	Gly	Asp	Asn	Ser	Ala	Gly	Tyr	Leu	Thr	Val	Pro	Leu	Arg	Pro	
173			235						240					245			
175	ttg	acc	att	ggg	aag	gag	gtg	act	atg	gat	gtt	cct	gct	cca	aat	gcc	884
176	Leu	Thr	Ile	Gly	Lys	Glu	Val	Thr	Met	Asp	Val	Pro	Ala	Pro	Asn	Ala	
177			250					255					260				
179	cca	gga	gtg	agg	ctg	cag	ctc	aag	gca	gag	ggc	tgc	cct	gag	gag	ctg	932
180	Pro	Gly	Val	Arg	Leu	Gln	Leu	Lys	Ala	Glu	Gly	Cys	Pro	Glu	Glu	Leu	
181		265					270					275					
183	gcc	gtg	cac	ctg	ggc	ttc	aat	ctc	tgt	gca	gag	gag	cag	gcc	ttc	ctg	980
184	Ala	Val	His	Leu	Gly	Phe	Asn	Leu	Cys	Ala	Glu	Glu	Gln	Ala	Phe	Leu	
185		280				285						290					
187	agc	agg	agg	aag	cag	gtg	gtg	gcc	aag	gcc	ctg	aag	cag	gcc	ctg	cag	1028
188	Ser	Arg	Arg	Lys	Gln	Val	Val	Ala	Lys	Ala	Leu	Lys	Gln	Ala	Leu	Gln	
189	295				300					305				310			
191	ctg	gac	aga	gac	ctg	cag	gag	gat	gag	gta	ccc	gtt	gtg	ggc	atc	atg	1076
192	Leu	Asp	Arg	Asp	Leu	Gln	Glu	Asp	Glu	Val	Pro	Val	Val	Gly	Ile	Met	
193				315						320				325			
195	gcc	aca	gga	gga	ggt	gcc	egg	gcc	atg	acc	tca	ctc	tac	ggc	cac	cta	1124
196	Ala	Thr	Gly	Gly	Gly	Ala	Arg	Ala	Met	Thr	Ser	Leu	Tyr	Gly	His	Leu	
197			330						335					340			
199	ttg	gcc	ttg	cag	aag	ctg	ggc	ctc	cta	gac	tgt	gtg	acc	tac	ttc	agt	1172
200	Leu	Ala	Leu	Gln	Lys	Leu	Gly	Leu	Leu	Asp	Cys	Val	Thr	Tyr	Phe	Ser	

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201	345	350	355	
203	ggc atc tct	ggc tct acg	tgg aca atg gcc cac	ctg tac ggg gac cct 1220
204	Gly Ile Ser	Gly Ser Thr	Trp Thr Met Ala His	Leu Tyr Gly Asp Pro
205	360	365	370	
207	gag tgg tcg	cag agg gac	ctg gag gga cct atc	aga tac gcc cgg gag 1268
208	Glu Trp Ser	Gln Arg Asp	Leu Glu Gly Pro	Ile Arg Tyr Ala Arg Glu
209	375	380	385	390
211	cac ctg gcc	aag agc aag	ctg gag gtc ttt	tcc cca gag cgc ctg gcg 1316
212	His Leu Ala	Lys Ser Lys	Leu Glu Val Phe	Ser Pro Glu Arg Leu Ala
213		395	400	405
215	agc tac cgc	cgg gag ctg	gag ctg cgg gct	gag cag ggc cac ccc acg 1364
216	Ser Tyr Arg	Arg Glu Leu	Glu Leu Arg Ala	Glu Gln Gly His Pro Thr
217		410	415	420
219	acc ttt gtg	gac ctg tgg	gcg cta gtg ctg	gag tcc atg ctg cac ggc 1412
220	Thr Phe Val	Asp Leu Trp	Ala Leu Val Leu	Glu Ser Met Leu His Gly
221		425	430	435
223	cag gtg atg	gat cag aag	ctg tca gga cag	aga gcc gcc ctg gaa cgg 1460
224	Gln Val Met	Asp Gln Lys	Leu Ser Gly Gln	Arg Ala Ala Leu Glu Arg
225		440	445	450
227	ggt cag aac	cct ctg ccc	ctc tac ttg agc	ctc aat gtc aaa gag aac 1508
228	Gly Gln Asn	Pro Leu Pro	Leu Tyr Leu Ser	Leu Asn Val Lys Glu Asn
229	455	460	465	470
231	aat ctg gag	aca ctg gac	ttc aag gag tgg	gtt gag ttc tcc ccc tat 1556
232	Asn Leu Glu	Thr Leu Asp	Phe Lys Glu Trp	Val Glu Phe Ser Pro Tyr
233		475	480	485
235	gag gtc ggt	ttc ctg aag	tac ggg gcc ttc	gtc cct cct gag ctc ttc 1604
236	Glu Val Gly	Phe Leu Lys	Tyr Gly Ala Phe	Val Pro Pro Glu Leu Phe
237		490	495	500
239	ggc tcc gag	ttc ttc atg	gga cgg ctg	atg agg agg atc ccg gag ccc 1652
240	Gly Ser Glu	Phe Phe Met	Gly Arg Leu Met	Arg Arg Ile Pro Glu Pro
241		505	510	515
243	cgg atc tgc	ttt ctg gaa	gcc atc tgg agc	aac att ttc tcc ctg aac 1700
244	Arg Ile Cys	Phe Leu Glu	Ala Ile Trp Ser	Asn Ile Phe Ser Leu Asn
245		520	525	530
247	ctg ctg gat	gcc tgg tat	gac ctc acc agt	tct ggg gag tcc tgg aaa 1748
248	Leu Leu Asp	Ala Trp Tyr	Asp Leu Thr Ser	Ser Gly Glu Ser Trp Lys
249	535	540	545	550
251	cag cac atc	aag gac aag	acc agg agc tta	gag aag gag ccc ctg acc 1796
252	Gln His Ile	Lys Asp Lys	Thr Arg Ser Leu	Glu Lys Glu Pro Leu Thr
253		555	560	565
255	acc tcg ggg	acc tcc tcg	cgg ctg gag gcc	tcg tgg ctg cag cca ggc 1844
256	Thr Ser Gly	Thr Ser Ser	Arg Leu Glu Ala	Ser Trp Leu Gln Pro Gly
257		570	575	580
259	acg gcg ctg	gcc cag gca	ttt aaa ggc ttc	ctg aca ggc agg ccc ctc 1892
260	Thr Ala Leu	Ala Gln Ala	Phe Lys Gly Phe	Leu Thr Gly Arg Pro Leu
261		585	590	595
263	cac cag cgc	agc ccc aac	ttc ctc cag ggc	ctc cag ctg cac cag gac 1940
264	His Gln Arg	Ser Pro Asn	Phe Leu Gln Gly	Leu Gln Leu His Gln Asp
265		600	605	610

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267 tac tgt agc cac aaa gac ttc tcc acc tgg gca gac tac cag ctt gac 1988
268 Tyr Cys Ser His Lys Asp Phe Ser Thr Trp Ala Asp Tyr Gln Leu Asp
269 615 620 625 630
271 tcc atg ccc agc cag ctg acc ccc aag gag ccc cgg ctc tgc ctg gtg 2036
272 Ser Met Pro Ser Gln Leu Thr Pro Lys Glu Pro Arg Leu Cys Leu Val
273 635 640 645
275 gac gcc gcc tac ttc atc aac acc agc tct ccc tcc atg ttc cgg cca 2084
276 Asp Ala Ala Tyr Phe Ile Asn Thr Ser Ser Pro Ser Met Phe Arg Pro
277 650 655 660
279 ggc cgc agg ctg gac ctc atc ctc tcc ttc gac tac tcc cta tct gcg 2132
280 Gly Arg Arg Leu Asp Leu Ile Leu Ser Phe Asp Tyr Ser Leu Ser Ala
281 665 670 675
283 ccc ttc gag gca ctg cag cag acg gag ctg tac tgc cgg gcc cgg ggg 2180
284 Pro Phe Glu Ala Leu Gln Gln Thr Glu Leu Tyr Cys Arg Ala Arg Gly
285 680 685 690
287 ctg ccc ttc ccc cgg gtg gaa ccc agc cct cag gac cag cac cag cca 2228
288 Leu Pro Phe Pro Arg Val Glu Pro Ser Pro Gln Asp Gln His Gln Pro
289 695 700 705 710
291 agg gaa tgc cac ctc ttc tca gac ccc gcc tgc ccc gag gcc ccg atc 2276
292 Arg Glu Cys His Leu Phe Ser Asp Pro Ala Cys Pro Glu Ala Pro Ile
293 715 720 725
295 ctg ctg cac ttc ccg ctg gtc aat gcc tcc ttc aag gac cac tca gcc 2324
296 Leu Leu His Phe Pro Leu Val Asn Ala Ser Phe Lys Asp His Ser Ala
297 730 735 740
299 ccc ggt gtc cag cgc agc ccc gca gag ctc cag ggt ggc caa gtg gat 2372
300 Pro Gly Val Gln Arg Ser Pro Ala Glu Leu Gln Gly Gly Gln Val Asp
301 745 750 755
303 ctc acc ggg gcc acc tgc ccc tac acc ctg tcc aac atg acc tac aag 2420
304 Leu Thr Gly Ala Thr Cys Pro Tyr Thr Leu Ser Asn Met Thr Tyr Lys
305 760 765 770
307 gag gaa gac ttc gag cgc ctg ctg cgg ctc agt gac tac aac gtg cag 2468
308 Glu Glu Asp Phe Glu Arg Leu Leu Arg Leu Ser Asp Tyr Asn Val Gln
309 775 780 785 790
311 acc agc cag ggt gcc atc ctg cag gcc ctg agg acc gcg ctg aag cac 2516
312 Thr Ser Gln Gly Ala Ile Leu Gln Ala Leu Arg Thr Ala Leu Lys His
313 795 800 805
315 cgg act cta gag gcg agg cct cca agg gca cag acc tgaggttgct 2562
316 Arg Thr Leu Glu Ala Arg Pro Pro Arg Ala Gln Thr
317 810 815
319 cagaggctgc aggaccctcc agggcctgcg ggcataacct gatctgtage tgggctcagc 2622
321 cacaggcctt cctgggttgga gttctgggct ctcccaggcc tgggtggcct ctgtagctgg 2682
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325 agatgagttg aaaataaactt cgccaggcca gtgtgtagaa cagctgggtcc aaccagacag 2802
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333 ccacctcctc cctctctgtt ccttctctcc tttgtctctc tgctttccgt atccaagtct 3042
335 tgtacttggt taaatttatt cctaaatatt ttattctttt tgataagtgg agttactttc 3102
337 ttaatttcat ttagattatt cattgctatt ttatagaaat acaatggatt tttaaatggt 3162
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date